I. AMENDMENTS

In the specification:

Please replace the paragraph beginning on line 1 of page 2 with the following:

--Virus-specific T lymphocytes, along with neutralizing antibodies, are the mainstay of the antiviral immune defense in established viral infections. Whereas $CD8^+$ cytotoxic T cells eliminate virus-infected-cells, $CD4^+$ T helper cells are essential for the efficient regulation of the antiviral immune response. $CD4^+$ T helper cells recognize specific antigens as peptides bound to autologous HLA class II molecules (viral antigens or particles are taken up by professional antigen-presenting cells, processed to peptides, bound to HLA class II molecules in the lysosomal compartment, and transported back to the cell surface). Several observations support an important role of $CD4^+$ T cells in the elimination of HCV infection. Tsai *et al.*, 1997 Hepatology 25:449-458; Diepolder et al 1995 Lancet 346:1006-1007; Missale et al 1996 JCI 98: 706-714; Botarelli et al 1993; Gastro 104: 580-587; Diepolder et al 1997 J.Virol 71: 6011. Immunogenic peptides usually have a minimal length of 8-11 amino acids. However, since the peptide binding groove of HLA class II molecules seems to be open at both ends, longer peptides are tolerated. Thus peptides eluted from HLA class II molecules are typically in the range of 15-25 amino acids. HLA class II molecules are extremely polymorphic and each allele seems to have its individual requirements for peptide binding. Thus the HLA class II repertoire of a given individual determines which viral peptides can be presented to T cells. Recognition of the specific HLA-peptide complex by the T cell receptor accompanied by appropriate costimulatory signals lead to T cell activation, secretion of cytokines, and T cell proliferation.--

Please replace the paragraph beginning on line 24 of page 19 with the following:

--Another method of establishing percent identity in the context of the present

invention is to use the MPSRCH package of programs copyrighted by the University of Edinburgh, developed by John F. Collins and Shane S. Sturrok, and distributed by IntelliGenetics, Inc. (Mountain View, CA). From this suite of packages, the Smith-Waterman algorithm can be employed where default parameters are used for the scoring table (for example, gap open penalty of 12, gap extension penalty of one, and a gap of six). From the data generated, the "Match" value reflects "sequence identity." Other suitable programs for calculating the percent identity or similarity between sequences are generally known in the art, such as the alignment program BLAST, which can also be used with default parameters. For example, BLASTN and BLASTP can be used with the following default parameters: genetic code = standard; filter = none; strand = both; cutoff = 60; expect = 10; Matrix = BLOSUM62; Descriptions = 50 sequences; sort by = HIGH SCORE; Databases = non-redundant, GenBank + EMBL + DDBJ + PDB + GenBank CDS translations + Swiss protein + Spupdate + PIR. Details of these programs can be found on the world wide.--

In the claims:

Please amend claims 1 to 3 and 13 as follows:

1. (Amended) An isolated mutant non-structural ("NS") HCV polypeptide comprising a polypeptide having a deletion of more than 60 amino acids from the N-terminal portion of NS3, wherein said deletion functionally disrupts the catalytic domain of NS3 and further wherein said polypeptide comprises the C-terminal portion of NS3.

2. (Amended) The ~~polypeptide of~~ claim 1, wherein the deletion is at least 200 amino acids.